at a concentration of 2 x $10^{12}$ phage/mL. An anti-(His)5 antibody (Qiagen) was used as the capture target. See Example 22.--

Please replace the paragraph beginning at page 69, line 32, with the following rewritten paragraph:

--LV: GAGGGCAGCTGTGGCTTCGGTGGCGGTVVCVVCVVCVVCVVCV--

Please replace the paragraph beginning at page 78, line 30, with the following rewritten paragraph:

--Standard molecular biology techniques were used to construct a phagemid designated pS1290a. pS1290a is identical to phagemid pS349 (see Example 8) except that the open reading frame (ORF) under the control of the IPTG-inducible Ptac promoter (New England Biolabs) has been deleted and replaced by a new ORF. The new ORF encodes a fusion product consisting of the maltose binding protein signal peptide, followed by a Ser residue, followed by residues 2-50 of mature protein VIII of *E. coli* bacteriophage M13. The ORF is followed by two TAA stop codons, followed by sequence (CACCATCACCATCACCATGCG) (SEQ ID NO: 108) encoding a heptapeptide (HHHHHHA (SEQ ID NO. 280), hexaHis) flag or epitope tag, followed by two stop codons (TGATAA).--

Please replace the paragraph beginning at page 79, line 1, with the following rewritten paragraph:

--pS1290a was mutated using the method of Kunkel (Example 12). The two TAA stop codons and the first His codon following the protein VIII C-terminus were replaced by various numbers of Gly codons. Appropriately designed and named mutagenic oligonucleotides were used (*e.g.*, oligonucleotide *G-6* inserts six Gly codons). This resulted in the construction of a series of phagemids encoding ORFs designed to secrete protein VIII molecules with C-terminal fusions consisting of linkers containing varying numbers of Gly residues followed by a pentaHis flag (HHHHHA (SEQ ID NO. 279)). The number of Gly residues was varied from zero (*i.e.*, the polyHis flag was fused directly to the

protein VIII C-terminus) to 20. PentaHis flag display was measured by phage ELISA (Example 13) with an anti-(His)5 antibody (Qiagen) as the capture target (Fig. 13).--

Please replace the paragraph beginning at page 79, line 41, with the following rewritten paragraph:

--Linkers selected for display of a peptide fused to the C-terminus of protein VIII. The sequences shown were inserted between the final residue of protein VIII and a heptapeptide (HHHHHHA (SEQ ID NO. 280), referred to as a hexaHis flag). For each selectant, the DNA sequence is shown with the deduced amino acid sequence below. The numerical designation for each sequence is shown to the left.--

Please replace the paragraph beginning at page 80, line 24, with the following rewritten paragraph:

--This ORF was designed as follows. The first two residues were (Met-Ser) chosen to allow good translation initiation. This dipeptide was followed by a retrotranslation of residues 40-48 of mature protein VIII from M13 bacteriophage (KLFKKFTSK (SEQ ID NO. 282) retrotranslated to KSTFKKFLK SEQ ID NO. 283) which was in turn followed by a retrotranslation of protein VIII residues 1-20 (AEGDDPAKAAFNSLQASATE (SEQ ID NO. 285) retrotranslated to ETASAQLSNSAAKAPDDGEA (SEQ ID NO. 284)). To the C-terminus of this polypeptide was fused a nonapeptide (AAHHHHHHA (SEQ ID NO. 281)) hexaHis flag. Thus, this ORF consists of the dipeptide Met-Ser, followed by a retrotranslation of residues 1-48 of mature protein VIII with the central hydrophobic section (residues 21-30) deleted, followed by a hexaHis flag.--

Please replace the paragraph beginning at page 81, line 26, with the following rewritten paragraph:

--Phagemid pS1232a was digested with *Nsi*I and *Xba*I and a similarly digested DNA fragment encoding an hGH variant (hGH

supermutant, hGHsm) with improved afffinity for the hGH binding protein (hGHbp) was inserted. The phagemid was designated pS1239b; it contains an ORF encoding P12-1 followed by a tetrapeptide linker (Ala-Ala-Asp-Ala), followed by hGHsm as shown below. The protein product of the pS1239b ORF is depicted; it consists of P12-1, followed by a tetrapeptide linker (AADA (SEQ ID NO. 286)), followed by hGHsm. P12-1 was divided into six zones as indicated, and a library was constructed for each zone. In addition, a linker library was constructed in which random 14-residue peptides were inserted in the middle of the tetrapeptide linker as shown.--

Please replace the paragraph beginning at page 83, line 9, with the following rewritten paragraph:

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--ATG AGC AAG AGC ACT TTC AAA AAG TTT CTG
   M   S   K   S   T   F   K   K   F   L

AAA GTT TTT GTT TTT TCT GTT GAT GTT GAT
 K   V   F   V   F   S   V   D   V   D

AAT AAT TGG ATT TGG GCT GTC GGT ATT ATT
 N   N   W   I   W   A   V   G   I   I

TAC ATG CTC CTC GTG GAG GCG TCG CCC TGG
 Y   M   L   L   V   E   A   S   P   W

GCT GCT AAG GCG CCA GAC GAT GGT GAA GCT (SEQ ID NO. 124)
 A   A   K   A   P   D   D   G   E   A (SEQ ID NO. 33)--
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Please replace the paragraph beginning at page 84, line 23, with the following rewritten paragraph:

--Standard molecular biology techniques were used to construct a phagemid designated pS1428d. Phagemid pS1428d is similar to pS1290a, except that the ORF under the control of the IPTG-inducible Ptac

promoter (New England Biolabs) consists of the maltose binding protein signal peptide followed by the C-terminal domain of M13 protein III (Lowman *et al.*, (1991) *Biochemistry,* 30:10832). The method of Kunkel (Example 12) was used to fuse libraries to the C-terminus of the protein III C-terminal domain encoded by pS1428d. The libraries consisted of random linkers of various lengths followed by a hexaHis flag (HHHHHH (SEQ ID NO. 287)). The end result was libraries containing ORFs which encoded the C-terminal domain of protein III, followed by random polypeptide linker sequences, followed by the hexaHis flag. The lengths of the linkers were varied and depended on the mutagenic oligonucleotides used: oligonucleotides *UHg3-L6*, *UHg3-L8*, or *UHg3-L10* introduced linkers containing 6, 8, or 10 residues respectively. The diversities of the libraries were as follows: *UHg3-L6*, $3.5 \times 10^{10}$; *UHg3-L8*, $1.2 \times 10^{10}$; *UHg3-L10*, $2.8 \times 10^{10}$.--